

QY	601	KIVDEEEYERDENEFFALGEPKWMERGIS-----DTDRKLTMEEEARIAENKGPV.	654
FT	DOMAIN	169	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	170	POTENTIAL.
FT	DOMAIN	190	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	191	POTENTIAL.
FT	TRANSMEM	202	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	203	POTENTIAL.
FT	TRANSMEM	224	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	230	POTENTIAL.
FT	TRANSMEM	231	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	252	POTENTIAL.
FT	TRANSMEM	725	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	727	POTENTIAL.
FT	TRANSMEM	747	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	748	POTENTIAL.
FT	TRANSMEM	755	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	775	POTENTIAL.
FT	TRANSMEM	776	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	777	POTENTIAL.
FT	TRANSMEM	779	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	800	POTENTIAL.
FT	TRANSMEM	828	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	849	POTENTIAL.
FT	TRANSMEM	850	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	860	POTENTIAL.
FT	TRANSMEM	861	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	882	POTENTIAL.
FT	TRANSMEM	903	CYTOSMERIC (POTENTIAL).
FT	TRANSMEM	924	POTENTIAL.
FT	TRANSMEM	925	CYTOSMERIC (POTENTIAL).
FT	TRANSMEM	927	CALMODULIN-BINDING (BY SIMILARITY).
FT	TRANSMEM	929	ALPHA-1.
FT	TRANSMEM	140	BETA-1.
REPEAT	REPEAT	399	BETA-2.
REPEAT	REPEAT	534	ALPHA-2.
REPEAT	REPEAT	796	POLY-GLU.
FT	DOMAIN	645	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONRD	45	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBONRD	823	SEQUENCE 927 AA; 103162 MW; EAB35FF9620DBE69; CRC64;
Query	1	MAWLRLOPLTSRFLHGLUTVFLGLNLRAEGSGSVPSTGQNNEBCSGSSCKEGLV	60
Query	1	MAWLRLOPLTSRFLHGLUTVFLGLNLRAEGGLDROVPSAGQQNNECSGSDDCKEGLV	60
Query	1	PTWYPENPSLGDK1ARYVYFVALIYFGLGSIADRFMSAIEWTISOEREVTIKPN	120
Db	61	PTWYPENPSLGDK1ARYVYFVALIYFGLGSIADRFMSAIEWTISOEREVTIKPN	120
Db	61	PTWYPENPSLGDK1ARYVYFVALIYFGLGSIADRFMSAIEWTISOEREVTIKPN	120
Query	121	TSTTIRWNETVSNTLMALGSSAPEILLSIEVCCHGFIAGDGLGSTIGSSAARNFI	180
Db	121	TSTTIRWNETVSNTLMALGSSAPEILLSIEVCCHGFIAGDGLGSTIGSSAARNFI	180
Db	181	TGICCVVYIPDGERTKIKHLRFVFTAAWSFAYIWIMIILAVFSPGVQVWEGLTLFF	240
Db	181	TGICCVVYIPDGERTKIKHLRFVFTAAWSFAYIWIMIILAVFSPGVQVWEGLTLFF	240
Query	241	FPCVLLAWADKRLFPYKMHKYRDKHGRGIIETEGDHPKGIEDGKMNNSHELDGN	300
Db	241	FPCVLLAWADKRLFPYKMHKYRDKHGRGIIETEGDHPKGIEDGKMNNSHELDGN	300
Query	301	LYPLEGEKVDESTERREMIRLKOKOKEPKDQLVEMANLYALSHOOKSRAFTYQATR	360
Db	301	LYPLEGEKVDESTERREMIRLKOKOKEPKDQLVEMANLYALSHOOKSRAFTYQATR	360
Db	361	MWPGAGNLTKKHAEQAKASSNSEVHIDEPEDPISVKFFDCPSYCQLENCCAVLTVVR	420
Db	361	MWPGAGNLTKKHAEQAKTASNEVHIDEPEDPASKVFEDCPSYCQLENCCAVLTVVR	420
Query	421	KGGDMSKMYVQKTEDGSANAGADYBETEGTVLKGTEOKFSVGLDDDFEDEHF	480
Db	421	KGGDSKMYVQKTEDGSANAGADYBETEGTVLKGTEOKFSVGLDDDFEDEHF	480
Query	481	FVRLSNVIEEPEEGMPATNSLPLPRAVIALSPCAVATVILDDDHAGFTFECITH	540
Db	481	FVRLSNVIEEPEEGMPATNSLPLPRAVIALSPCAVATVILDDDHAGFTFECITH	540
Db	481	FVRLSNVIEEPEEGMPATNSLPLPRAVIALSPCAVATVILDDDHAGFTFECITH	540
Query	541	VSESGIMVVKVIRTSGARTVIVPFRVEGAKGGDEFDYGELEFKNDTETKIV	600
Db	541	VSESGIMVVKVIRTSGARTVIVPFRVEGAKGGDEFDYGELEFKNDTETKIV	600
Db	541	VSESGIMVVKVIRTSGARTVIVPFRVEGAKGGDEFDYGELEFKNDTETKIV	600
Db	661	GBHPKLEVIESYEKTTWDKLKITTNLALWVGTHSWRDOFMEAITSAGDEEDESG	720
Db	715	ERRLPSCFDYYWHFLTVFWKVLFAVCUPPTEXCHGWCFAVSLIGMLTATGDLASHFG	774
Db	721	ERRLPSCFDYYWHFLTVFWKVLFAVCUPPTEXCHGWCFAVSLIGMLTATGDLASHFG	780
Db	841	SVAIWALQOGEFHYSAGTIAFLSVLFTIFAVFCISVLYRRPHGGLGGPCKLA	894
Db	841	SVAIWALQOGEFHYSAGTIAFLSVLFTIFAVFCISVLYRRPHGGLGGPCKLA	900
Db	895	TWLFVSLWMLYLTFATLEYCYIKGF	921
Db	901	TWLFVSLWMLYLTFATLEYCYIKGF	927
RESULT	2		
NACL_CANFA			
ID	NACL_CANFA		
AC			
P2365;			
DT	01-NOV-1991 (Rel. 20, Created)		
DT	01-NOV-1991 (Rel. 20, Last sequence update)		
DE	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Sodium/calcium exchanger 1 precursor ($\text{Na}^{(+)}$ / $\text{Ca}^{(2+)}$) - exchange protein		
GN	SIC8A1.		
OS	Canis familiaris (Dog).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.		
OX	NBII_TAXID=9615;		
RN	[1]		
RP	SEQUENCE FROM N. A.		
RC	TISSUE:Heart;		
RX	MEDLINE=91047958; PubMed=1700476;		
RA	Nicoll D.A., Longoni S., Phillips K.D.;		
RT	"Molecular cloning and functional expression of the cardiac sarcoplasmal $\text{Na}^{(+)}\text{-Ca}^{2+}$ exchanger. ";		
RL	Science 250:562-565(1990).		
RN	[2]		
RP	SEQUENCE FROM N. A.		
RC	TISSUE:Heart;		
RX	MEDLINE=92152737; PubMed=1785844;		
RA	Nicoll D.A., Phillipson K.D.;		
RT	"Molecular studies of the cardiac sarcolemmal sodium-calcium exchanger. ";		
RL	Ann. N.Y. Acad. Sci. 639:181-188(1991).		
-	FUNCTION: RAPIDLY TRANSPORTS Ca^{2+} DURING EXCITATION-CONTRACTION COUPLING. (Ca^{2+}) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.		
CC	- ENZYME REGULATION: BY ATP.		
CC	- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.		
CC	- TISSUE SPECIFICITY: CARDIAC SARCOLEMMA.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	DRBML; M5725; ARAB62766.1; -.		
DR	PIR: A36417; A36417.		
DR	InterPro; IPR03644; Galx_beta.		

DR	InterPro: IPR004837; NaCa_Exemb.	QY	296 ---FLDNLNVLPLEGKEVD--- ESSREMIRILKDKKKHCKPEKDQLVEMANYYLASHQ
Pfam	PF01699; Na_Ca_Ex; 2.	QY	297 VDNFDLGALV-LEVDERQDDEBAREMARTELKKHCKPEREIQLEIANYQVLSQQQ
DR	PRINTS; PR01259; NaCAEXCHNGR.	QY	349 KSRAYFYTQATRMGTAGNILKHHAAQAKASSMSMVEHTDEP-DEPSKVFDPESYQC 407
SMART	SM0237; Calx_beta; 2.	QY	356 KSRAYFYTQATRMGTAGNILKHHAAQAKASSMSMVEHTDEP-DEPSKVFDPESYQC 415;
DR	TIGR00845; caca; 1.	Db	KW Transport; Antiport; Calcium transport; Sodium transport; KW transmembrane; Glycoprotein; Phosphorylation; Signal; KW Calmodulin-binding; Repeat. POTENTIAL.
FT	SIGNAL 1 32	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	CHAIN 1	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 72 93	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 94 133	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 134 155	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 155 167	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 168 188	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 189 199	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 200 222	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 223 225	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 226 249	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 250 769	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 770 789	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 790 796	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 797 819	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 820 821	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 822 840	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 841 871	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 872 892	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 893 903	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 904 924	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 925 941	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 942 958	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 959 970	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	TRANSHEM 971 982	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN 983 993	Db	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
REPEAT	178	Db	ALPHA-1.
FT	REPEAT 407 478	Db	EXTRACELLULAR (POTENTIAL).
FT	REPEAT 539 609	Db	POTENTIAL.
FT	REPEAT 839 875	Db	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 236 270	Db	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN 251 281	Db	POTENTIAL.
FT	DOMAIND 282 318	Db	CALMODULIN-BINDING (POTENTIAL).
FT	MOD_RES 389 389	Db	POLY-ASP.
FT	CARBOHYD 41 41	Db	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD 157 157	Db	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 866 866	Db	N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE	970 AA; 108004 MW;	Db	BBDGCC584846AB08 CRC64;
Q	Query Match	RESULT 3	
Q	Best Local Similarity 69.2%; Pred. No. 5 3e-219; Length 970; Matches 677; Conservative 109; Mismatches 127; Indels 65; Gaps 10;	NACL_FELCA	
Oy	1 MAWLRLOQPLTAFLHLGGLTFLF--LNGLRAEGSGSDVPSITGGNNECSGSSDKEGV 58	ID	NACL_FELCA STANDARD; PRT; 970 AA.
Db	1 MQLQRLIPTFSMGLCHLLAVALLFSHVLDISATEMEEGEGNETGE---CTGSYCKKGV 56	AC	
Oy	5 ILPIWIPPEPNPSLGDKARVIVFVALIVFVALIMFLGVSIAIDRPMASIEVTSQERETIKKP 118	DT	P48767; P79174; 01-FEB-1996 (Rel. 33, Created)
Db	57 ILPIWIPQDPSFGDKIARATVYFVAMWYMFGLGSITIADRFMSIEVTSQEETIKKP 116	DT	01-FEB-1996 (Rel. 33, Last sequence update)
Oy	119 GETSTTRIRVNETVSNTLMALGGSSAPEILSILIEVGHGFTAGDGLGSTVGSAAFM 178	DT	15-JUN-2002 (Rel. 41, Last annotation update)
Db	117 GETTKTIVRWNNTVSNTLMALGGSSAPEILSIVIEVGHNFTAGDGLGSTVGSAAFM 176	DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).
Oy	179 FILIGCVVYDGERKIKHURFFITAANSIFAYIWLYMLAVSPGWVQWEGCLLT 238	DE	GN G8A1 OR NCX1.
Db	177 FIIAIQCVVYDGERKIKHURFFITAANSIFAYIWLYMLAVSPGWVQWEGCLLT 236	OS	Felis silvestris catus (Cat); Bavarota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
Oy	239 EFPFPVCULLAWADKRLFYKMKKVRDKHIGLITTEGDPHKG--IEMDGKMINSH 295	OC	Medline: 6250114; PubMed: 8659865; NCBI_TAXID=9885; RN [2]
Db	237 EFPFPVCUFFAWADRRLFLFYKVKRAGKORGMIHEGRPPSSTEIENDKGVNISH 296	OX	Mcermott D.E., Rozich J.D., Kent R.L., Cooper G.; "The exchanger and cardiac hypertrophy;" Ann. N.Y. Acad. Sci. 779:489-501(1996).

RX MEDLINE=97269065; PubMed=9111065;
 RA Barnes K.V., Cheng G., Dawson M.M., Menick D.R.;
 RT "Cloning of cardiac, kidney, and brain promoters of the feline ncx1
 gene."
 RL J. Biol. Chem. 272:11510-11517(1997).
 CC -I- FUNCTION: RANDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
 COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
 SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
 -I- ENZYME REGULATION: BY ATP.
 -I- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 -I- TISSUE SPECIFICITY: CARDIAC SARCOLEMMA.
 CC
 DR EMBL; L35846; AAB41941.1; -.
 DR InterPro; IPR003644; Calk_beta.
 DR InterPro; IPR004837; NaCa_Exemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR Pfam; PF03160; Calx_beta; 2.
 DR PRINTS; PRO1259; NACEXCHNGR.
 DR SMART; SM00237; calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32
 FT DOMAIN 33 970
 FT DOMAIN 33 71
 FT TRANSMEM 72 93
 FT DOMAIN 94 133
 FT TRANSMEM 134 155
 FT DOMAIN 156 167
 FT TRANSMEM 168 188
 FT DOMAIN 189 199
 FT TRANSMEM 200 222
 FT DOMAIN 223 225
 FT TRANSMEM 226 249
 FT DOMAIN 250 769
 FT TRANSMEM 770 795
 FT DOMAIN 790 797
 FT TRANSMEM 820 821
 FT DOMAIN 822 840
 FT TRANSMEM 841 871
 FT DOMAIN 872 893
 FT TRANSMEM 893 904
 FT DOMAIN 924 941
 FT TRANSMEM 942 958
 FT DOMAIN 959 970
 FT DOMAIN 251 270
 FT REPEAT 138 178
 FT REPEAT 407 478
 FT REPEAT 539 609
 FT REPEAT 839 875
 FT DOMAIN 236 239
 FT DOMAIN 689 692
 FT DOMAIN 755 760
 FT MOD_RES 389 389
 FT CARBOHYD 41 41
 FT CARBOHYD 157 157
 FT CONFLICT 21 21
 FT CONFLICT 113 113
 SQ SEQUENCE 970 AA; 108004 MW; 2402F02DE35Dm-057 CRC64;

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 or send an email to license@isb-sib.ch).

Query Match	71.8%	Score 3442.5;	DB 1;	Length 970;
Best Local Similarity	69.3%	Pred. No. 1..1e-218;		
Matches	678;	Conservative	126;	Indels 67; Gaps 12;
QY	1	MAWLRQPLTSFLHGLGLTVF-LFLNGLRAEAGGGDVPSGONNES-CSGSDCKEG	57	
Db	1	MIRLRLSPFTSFGFH--LLAFVPLLESHVDLI--SADTEMEGEENETGCCTGSYCKKG	55	
QY	58	VILPIWYPENPNSLGDKITAARTVYVALLYMFLGVSIATDRMASIVITQEREVTIKP	117	
Db	56	VILPINERQDFSGDKIARATVYFVANVYMLGVSIAIDRMSSIEVITOQEKETIKKP	115	
QY	118	NGETSTUTIYWNNTYSNLTMALGSAPEILSLIEVGSGIFAGDLGSTIVSAEN	177	
Db	116	: : : : : : : : : : :	175	
QY	178	MTIIGCVVYIPDGGERKIKHLRVPTAAWSAISFYWLYMILAVFSPIWQWEGLT	237	
Db	176	MELIAACVYVYVPDGETERKIKHLRVFTAAWSAISFYTWLWILSVISPGVYEVNEGLT	235	
QY	238	LFPPVCPVLAQWAKDRKLFFYKYMHKRYTKHRGILTEBGDHPKG--IEMDGKMNNS	294	
Db	236	FFFFPICVCPVFAWADRRLFKIVKYKRYRAGKQGMIEHECDRPSKTEIEMDSKVNS	295	
QY	295	H---FLDGNLPLEGKVD---ESREMRTRIKDKOKRKEKDJDOLVEMANYALSHO	347	
Db	296		354	
QY	348	OKSRAFYRIQATRMMTGAGNTIKKHAEQAKASSAEVHDEPE-DFISVFFPCSY	406	
Db	355	QKSRAFYRIQATRMMTGAGNTIKKHAEQAKASSAEVHDEPE-DFISVFFPCSY	406	
QY	407	CLENCGAVLTLVVKRGDMMSKMYVKTEDSANAGADYFFTEGVVLKPGETOKEFSV	466	
Db	415	CLENCGAVLTLVVKRGDMMSKMYVKTEDSANAGADYFFTEGVVLKPGETOKEFSV	474	
QY	467	GTIDDDFEEDBHFVFLYRNTRIEESQEPQEMPAFFNPLSLPRAVLASPCVATVILDQ	526	
Db	475	GIDDDFEEDBHFVFLYRNTRIEESQEPQEMPAFFNPLSLPRAVLASPCVATVILDQ	531	
QY	527	DHAGIFIFECOPTHVBSIGNEVKURTSCARGTVIPPFRTVEGPAKGGEDFDTYG	586	
Db	532	: : : : : : : : : : :	591	
QY	587	DRAGIFIFECOPTHVBSIGNEVKURTSCARGTVIPPFRTVEGPAKGGEDFDTYG	591	
Db	592	LEFKNDETVKTRVKVDEEYERQENFFALGEPKMERG-----	627	
QY	628	-----ISDVTDRK-LTMEEEAKRKAEMKGKVGKGEHKLVE	662	
Db	652	LYQQPVPERVKVHAREHPITPSTVITAECDAKPLSKEEERRIAMGRPTLGEKTLEY	711	
QY	663	ITEESTEFKTVTDKLKTTNLALVGTHSWNDOMFTAITYSAAGDBEDDSEGEERLPSCE	722	
Db	712	: : : : : : : : : : :	771	
QY	723	TEESTEFKTVTDKLKTTNLALVGTHSWNDOMFTAITYSAAGDBEDDSEGEERLPSCE	722	
Db	772	DYVMHELTIVFKVLFKVFVLFKVFVLPTEYWNGWACTFVSLIMIGLAFISGLASHFTGKDS	831	
QY	783	VIAVVVAFAFGSPVDPASKAALQWYADASIGNVGSNAVNLGIGLAWSVAIYWA	842	
Db	832	VIAVVVAFAFGSPVDPASKAALQWYADASIGNVGSNAVNLGIGLAWSVAIYWA	891	
QY	843	LOGOEHVHSAGTLAFSTVLTFAFVCSIVYLRRPHLGEGPGRCLQIATWLFWV	902	
Db	892	ANGEQFRVSPGTLAFSTVLTFAFVCSIVYLRRPHLGEGPGRCLQIATWLFWV	951	
QY	903	WLYLIEATLERYCYIKGF	921	
Db	952	WLYLIEFSSLRYCHIKGF	970	

RESULT 4

NAC1_HUMAN STANDARD: PRT; 973 AA.

ID NAC1_HUMAN PRT; 973 AA.

AC P32418; Q9UBL8; Q9IKX6; 095849; Q9UDN1; Q9UDN2;

DT 01-OCT-1993 (Rel. 27, created)

DT 16-OCT-2002 (Rel. 41, last sequence update)

DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).

GN SLC8A1 OR NCX1 OR CNC.

OS Homo sapiens (Human).

OC Mammalia; Eutheria; Chordata; Craniata; vertebrata; Euteleostomi;

OC Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi;

OX NCBI_TAXID=9606;

RN [1]

SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Heart;

RX MEDLINE=92262521; Pubmed=1374913;

RX Komuro I., Wenniger K.E., Phillipson K.D., Izumo S.;
"Molecular cloning and characterization of the human cardiac Na+/Ca2+ exchanger cDNA";

RT Proc. Natl. Acad. Sci. U.S.A. 89:4769-4773(1992).

RN [2]

SEQUENCE FROM N.A. (ISOFORMS 3 AND 7).

RX MEDLINE=21136311; Pubmed=11241183;

RX Van Eylen F., Boilen A., Herchuelz A.;
"Na+/Ca2+ exchanger variants in cultured human retinal pigment epithelium";

RT J. Endocrinol. 168:517-526(2001).

RN [3]

SEQUENCE OF 1-603 FROM N.A. (ISOFORM 7).

RX Margioli N.J., Chen W., Wang Q., Kennedy B.G.;
"Na+/Ca2+ exchanger isoforms in pancreatic islet cells";

RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

SEQUENCE OF 1-603 FROM N.A. (ISOFORM 7).

RX Rohlfing T., Strommatt C., Soronce D., Moody T.;
Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [5]

SEQUENCE OF 850-973 FROM N.A.

RX Kozlowski A., Stoneking T., Hawkins M., Le T.;
Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

RN [6]

SEQUENCE OF 459-681 FROM N.A. (ISOFORM 10).

RX Lundquist P., Lundgren T., Grifflin-Linde A., Linde A.;
Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.

CC -1- ENZYME REGULATION: BY ATP.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.

CC -1- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS; 1(NAC1)/NCX1.1 (SHOWN HERE), 3(NAC1/NCX1.3, 7(NAC1/NCX1.7 AND 10(NAC10/NCX1.10; ARE PRODUCED BY ALTERNATIVE SPlicing.

CC -1- TISSUE SPECIFICITY: CARDIAC SARCOMERMA.

CC

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DR M91368; AAA5702_1; -;

DR EMBL; AF08389; AF08988_1; -;

DR EMBL; AF128524; AF26362_1; -;

DR EMBL; AF007281; AF19237_1; -;

DR EMBL; AF010724; AF19235_1; -;

DR EMBL; AF115505; AF17213_1; -;

DR PIR; S32815; S32815.

DR Genew; HGNC;11068; SLC8A1.

DR MIM: 182305; -;

DR InterPro; IPR003644; Calx_beta.

DR InterPro; IPR00437; Naca_Exemb.

DR InterPro; IPR004836; Na,Ca_Ex.

DR Pfam; PF01699; Na,Ca_Ex; 2.

DR Pfam; PF01699; Na,Ca_Ex; 2.

DR SMART; SM00237; NACAEXHNGR.

DR TIGRFAM; TIGR0845; caca; 1.

KW Transport; Antiport; Calcium transport; Sodium transport;

KW Transmembrane; Glycoprotein; Phosphorylation; Signal;

KW Calmodulin-binding; Repeat; Alternative splicing;

KW SIGNAL 1 35

FT CHAIN 36 973

FT DOMAIN 74 36

FT TRANSMEM 75 96

FT DOMAIN 97 136

FT TRANSMEM 137 158

FT DOMAIN 159 170

FT TRANSMEM 171 191

FT DOMAIN 192 202

FT TRANSMEM 203 225

FT DOMAIN 226 228

FT TRANSMEM 229 252

FT DOMAIN 253 272

FT TRANSMEM 773 792

FT DOMAIN 793 799

FT TRANSMEM 800 822

FT DOMAIN 823 824

FT TRANSMEM 825 843

FT DOMAIN 844 874

FT TRANSMEM 875 895

FT DOMAIN 905 906

FT TRANSMEM 907 927

FT DOMAIN 928 944

FT TRANSMEM 945 961

FT DOMAIN 962 973

FT DOMAIN 254 273

FT REPEAT 141 181

FT REPEAT 410 481

FT REPEAT 542 612

FT REPEAT 842 878

FT DOMAIN 239 242

FT DOMAIN 692 695

FT DOMAIN 759 763

FT MOD_RES 392 392

FT CARBOHYD 44 44

FT CARBOHYD 160 160

FT CARBOHYD 869 869

FT VARSPLIC 605 613

FT VARSPLIC 619 645

FT VARSPLIC 652 656

FT VARSPLIC 652 679

FT SEQUENCE 973 AA; 108546 MN; 17DFC1B15921DB CRC64;

OY 1 MAWFLRQLPQPLSAFLHFGFLVFLVFL--LNGRLRAEAGGSDGDPSTGCONNECSGSSDCKEV 58

Db 4 MRRSLSPFSMGFLLVLSLFSHVDAVTEMEEGEGNETE---CTGSVYCKGV 59

OY 59 ILPWPWPEPNPLSGKIAKRYIVWVALINFLGVSIIADRMASIEVTQSQREVITKKR 118

Db 60 ILPWPQPSFGDKIARATVYEVAMVYELGVSIIADRMSSEVITSOEKETIKRN 119

OY 119 GETSTTIRWNETVSNLTMALGSSAPBLLSIEVGHGFTAGDGPFSTIVGSAAFNM 178

Db 120 GETTKTIVWNETVSNLTMALGSSAPBLLSIEVGHNFTAGDGFPTIVGSAAFNM 179

OY	179	FIIGICVVYIPDGETRKIKHLRVEFTITAAMSIFAYIWLMILAVFSPGVWQWNGCLTL	238	RP SEQUENCE FROM N. A.
Db	180	FIIALCVVYIPDGETRKIKHLRVEFTITAAMSIFAYIWLMILAVFSPGVWQWNGCLTL	239	RC TISSUE-Heart;
Db	239	FFFFPVCLLWNAADKULFYMMKKYRTDKHRRGILIEETGDHPRG--IEMDGKNNSH	295	RX MEDLINE-95078257; PUBMED-7986817;
Qy	240	FFFPICVVFAAWADRRLFYKYVKYRAGKORGMIIEHSGDRPPSKTEIEMDGKVNSH	299	RR Tsuria, I., Bessohn, M.M., Li, Z., Nicoll, D.A., Phillipson, K.D.;
Db	296	--EFLGNLVPLEGKEVD---ESREMIRILDKLQKHEDKDOLVLEMANVYALSHQ	348	RT "Molecular cloning and functional expression of the guinea pig Na(+)-Ca(2+) exchanger.";
Db	300	VENFLDGLAVLEVDENDQDDEERAREMARILKELQKHPDEIQOLIELANYQLSQO	358	RL Bloch, J. Blophys. Acta 1396:97-99;(1994).
Qy	349	KSRAFVRIQATRMIGAGNIKKHAEQAKKASMSEVHTDEP-EPIKVFFDCSYC	407	CC -I- FUNCTION: RAPIDLY TRANSPORTS Ca(2+) DURING EXCITATION-CONTRACTION
Db	359	KSRAFVRIQATRMIGAGNIKKHAEQAKKASMSEVHTDEP-EPIKVFFDCSYC	418	CC COUPLING: Ca(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
Qy	408	LENCGAVLLTVWRKGDDMSKTMVYDKTERCSANAGADYERTEGTWVLKGETKEFVG	467	CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
Db	419	LENCGAVLLTVWRKGDDMSKTMVYDKTERCSANAGADYERTEGTWVLKGETKEFVG	478	CC -I- ENZYME REGULATION: BY ATP.
Db	468	IIDDDIDEEDHFYVLSNYRVEEOPEGMPAENSLPLPRAVLASPCVATWILDD	527	CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
Db	479	IIDDDIDEEDHFYVLSNYRVEEOPEGMPAENSLPLPRAVLASPCVATWILDD	535	CC -I- TISSUE SPECIFICITY: CARDIAC SARCOLEMA.
Oy	528	HAGIFFECDTIHNSISIGMEVKVARTSGARGTVIPFRTEGAKGGDFDFTYGEI	587	DR InterPro; IPR04837; Na,Ca_Exemb.
Db	536	HAGIFFEFPEPYTHVSISIGMEVKVLTSCARGNIVPYKTECTARGGEDDETCGEL	595	DR InterPro; IPR04836; Na,Ca_Ex.
Qy	588	EFKNDENETVKTRVKVDEEEVERQENFFIALGEPKHMERG-----	627	DR PFam; PF03160; calx-beta_2.
Db	596	EFQNDENEVKTSKVIDEEYEKNTFFLEGEPRLEMSEKKALLNELOGFTTGKL	655	DR PRINTS; PRO1259; Na,CHEXCHNGR.
Qy	628	-----ISDVTDRK-LTMEEEEAKRRAENGKPVLGHEKLEV	663	DR SMART; SM0237; Calx_beta_2.
Db	656	FGQPVPRVKVHAREHPLSTVITIADEYDDQKPLSKREEERIAEMGRPILEHKLEV	715	DR TIGRFAMs; TIGR0845; caca_1.
Oy	664	IEESYERKTVDLKLKTTNLALVGHSHWDQFEMENTVSAGGDEDDESEGERLPSCED	723	KW Transport; Antipart; Calcium transport; Sodium transport;
Db	716	IEESYERKTVDLKLKTTNLALVGHSHWDQFEMENTVSAGGDEDDESEGERLPSCED	775	KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
Qy	724	YVMHFLTVFWKVLFACVPPTEYCHGACFAVSIILIGMTAIGDLASHHGCTIGLDSV	783	KW Calmodulin-binding; Repeat.
Db	776	YVMHFLTVFWKVLFAVPPTEYCHGACFAVSIILIGMTAIGDLASHHGCTIGLDSV	835	FT CHAIN 1 32 POTENTIAL.
Oy	784	TAVVVFVAGHTSVPDTFASKAAALQDYADASIGNYTGSNAUNVFLGIGLAWSYAIW	843	FT DOMAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
Db	836	TAVVVFVAGHTSVPDTFASKVATODYADASIGNYTGSNAUNVFLGIGLAWSYAIW	895	FT TRANSMEM 72 93 EXTRACELLULAR (POTENTIAL).
Oy	844	QOQEHHVSAGTLASFVLTIFAVFCISVLLYRRPHLGGELGGPRCKLAFTWFLW	903	FT TRANSMEM 94 133 POTENTIAL.
Db	896	NGEOFKVSPGTLAFLSVLTFIFAFINVGVLVYRRPPEIGELGGPRCKLAFTSCLFLW	955	FT TRANSMEM 134 155 CYTOPASIC (POTENTIAL).
Qy	904	LIVLFATLEAYCYIKGF	921	FT TRANSMEM 156 167 EXTRACELLULAR (POTENTIAL).
Db	956	LLYIFFSSLEAYCHIKGF	973	FT TRANSMEM 168 188 EXTRACELLULAR (POTENTIAL).
RESULT 5				
ID	NACL_CAVPO	STANDARD:	PRT:	970 AA.
ID	NACL_CAVPO			
AC	P48766;			
DT	01-FEB-1996 (Rel. 33, Created)			
DT	01-FEB-1996 (Rel. 33, Last annotation update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).			
DE	SLC8A1.			
OS	Cavia porcellus (Guinea Pig);			
OC	Eukaryota; Metzoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.			
OX	NCBI_TaxId-1011;			
RN	[1]			

RESULT 6	
ID	NAC1_RAT
AC	NAC1_RAT
DT	01-JUL-1993 (Rel. 26, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	sodium/calcium exchanger 1 precursor ($\text{Na}^{(+)}$ / $\text{Ca}^{(2+)}$ -exchange protein 1).
GN	SLC8A1 OR NCX1.
OS	rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Rattus.
OX	NCBI_Taxid=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Heart;
RX	MEDLINE=93138118; PubMed=8422940;
RA	Low W., Kasir J., Rahamimoff H.;
RT	"Cloning of the rat heart $\text{Na}^{(+)}$ - Ca^{2+} exchanger and its functional expression in HeLa cells";
RL	FEBS Lett. 316:63-67(1993);
RN	[2]
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC	TISSUE=Brain;
RX	MEDLINE=9302244; PubMed=8454039;
RA	Furman I., Cook O., Kasir J., Rahamimoff H.;
RT	"Cloning of two isoforms of the rat brain $\text{Na}^{(+)}$ - Ca^{2+} exchanger gene and their functional expression in HeLa cells";
RL	FEBS Lett. 319:105-109(1993);
RN	[3]
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC	STRAIN=Sprague-Dawley; TISSUE=Kidney cortex;
RX	MEDLINE=94253030; PubMed=8195112;
RA	Lee S.-L., Yu A.S.-L., Lytton J.;
RT	"Tissue specific expression of $\text{Na}^{(+)}$ - Ca^{2+} exchanger isoforms.";
RL	J. Biol. Chem. 269:1849-14852(1994).
RN	[4]
RP	TISSUE SPECIFICITY.
RC	STRAIN=Sprague-Dawley;
RX	MEDLINE=96394663; PubMed=8798769;
RA	Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J., Williamson K.D.;
RT	"Cloning of a third mammalian $\text{Na}^{(+)}$ - Ca^{2+} exchanger, NCX3.;"
J. Biol. Chem. 271:24914-24921(1996).	
CC	- FUNCTION: RAPIDLY TRANSPORTS Ca^{2+} DURING EXCITATION-CONTRACTION COUPLING. $\text{Ca}^{(2+)}$ IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC	- ENZYME REGULATION: BY ATP.
CC	- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC	- ALTERNATIVE PRODUCTS: 5 isoforms; heart/NAC1 (shown here), brain 1/NACA5, kidney 2/NACA4, kidney 1/NACAT7 and kidney 2/NACA3; are produced by alternative splicing.
CC	- TISSUE SPECIFICITY: CARDIAC SARCOLEMMA OR BRAIN, AND SPLEEN.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation, the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.html or send an email to license@isb-sib.ch).
DR	EMBL; X68191; CAA48273.1; -
DR	EMBL; X68812; CAA48707.1; -
DR	EMBL; X68913; CAA48708.1; -
DR	EMBL; U04933; AAC319952.1; -
DR	EMBL; U04934; AAC191914.1; -
DR	EMBL; U04936; AAC19125.1; -
DR	PIR; S25552; S25552.
DR	PIR; S28833; S28833.
INTERPRO	IPR03641; Calx_beta.
INTERPRO	IPR004837; Naca_Exmemb.

DR	InterPro: IPR004836; NA-Ca_Ex.	Db	114 KPNGETTKTVIWNESVSNLTMAGSSABILSVIEVGHNFWAGDGLGPSTVGSAA 173
Pfam	PRO1699; Na_Ca_Ex; 2.	Db	174 FNMFTITGICVYVPPDGETRKTHRLRFFTAWSIFAYIWLYMLAVFSGPVWQWEGL 235
Pfam	PF03160; CaX_beta; 2.	Db	176 FNMFTITGICVYVPPDGETRKTHRLRFFTAWSIFAYIWLYMLAVFSGPVWQWEGL 293
PRINTS	PRO1239; NACAECHNGR.	Db	177 SMART; SM00237; CaX_beta; 2.
SMART	TIGR00845; calca; 1.	Db	178 TIGRFAMS; TIGR00845; calca; 1.
DR	Transport: Antipor; Calcium transport;	Db	179 Transport: Glycoprotein; Phosphorylation; Signal;
KW	transmembrane; Glycoprotein; Calmodulin-binding; Repeat; Alternative splicing.	Db	180 Calmodulin-binding; Repeat; Alternative splicing.
KW	Calmodulin-binding; Repeat; Alternative splicing.	Db	181 Calmodulin-binding; Repeat; Alternative splicing.
FT	SIGNAL 1	Db	182 SIGNAL 1
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FT	TRANSMEM 1185	Db	416 TRANSMEM 1185
FT	TRANSMEM 1186	Db	417 TRANSMEM 1186
FT	TRANSMEM 1187	Db	418 TRANSMEM 1187
FT	TRANSMEM 1188	Db	419 TRANSMEM 1188
FT	TRANSMEM 1189	Db	420 TRANSMEM 1189
FT	TRANSMEM 1190	Db	421 TRANSMEM 1190
FT	TRANSMEM 1191	Db	422 TRANSMEM 1191
FT	TRANSMEM 1192	Db	423 TRANSMEM 1192
FT	TRANSMEM 1193	Db	424 TRANSMEM 1193
FT	TRANSMEM 1194	Db	425 TRANSMEM 1194
FT	TRANSMEM 1195	Db	426 TRANSMEM 1195
FT	TRANSMEM 1196	Db	427 TRANSMEM 1196
FT	TRANSMEM 1197	Db	428 TRANSMEM 1197
FT	TRANSMEM 1198	Db	429 TRANSMEM 1198
FT	TRANSMEM 1199	Db	430 TRANSMEM 1199
FT	TRANSMEM 1200	Db	431 TRANSMEM 1200
FT	TRANSMEM 1201	Db	432 TRANSMEM 1201
FT	TRANSMEM 1202	Db	433 TRANSMEM 1202
FT	TRANSMEM 1203	Db	434 TRANSMEM 1203
FT	TRANSMEM 1204	Db	435 TRANSMEM 1204
FT	TRANSMEM 1205	Db	436 TRANSMEM 1205
FT	TRANSMEM 1206	Db	437 TRANSMEM 1206
FT	TRANSMEM 1207	Db	438 TRANSMEM 1207
FT	TRANSMEM 1208	Db	439 TRANSMEM 1208
FT	TRANSMEM 1209	Db	440 TRANSMEM 1209
FT	TRANSMEM 1210	Db	441 TRANSMEM 1210
FT	TRANSMEM 1211	Db	442 TRANSM

QY	784	TAVVEAAGFTSPDPTFASKAKLQLDYADDASIGNYTGNSANVNFGLGLWVAIYLWAL	843
Db	833	TAVVFVALGTSVPDTFASKAVTQDQYADASIGNYTGNSANVNFGLGLWVAIYLWAL	892
QY	844	OQEAEHVSAGTAFSTVLFTIFAFVCISVLLYRRRLHGELGGPRCKLATWLESLW	903
Db	893	NGEOKVYSPGTLSFTVLTETAFAFINGVLYRREPEIGSGLGGPRPAKILSCLVLLW	952
RESULT 8			
NAC1_MOUSE			
ID	NAC1_MOUSE	STANDARD;	PRT;
AC	P70414;		970 AA.
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DE	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).		
DS	SLC8A1 OR NOX.		
OC	Eukaryota; Metazoa; Chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.		
OC	NCBItaxid=10090;		
RN	[1]		
SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6;		
RX	MEDLINE=96250070; PubMed=8659820;		
RA	Kim T., Lee C.O.,		
RT	"Cloning of the mouse cardiac Na(+) -Ca2+ exchanger and functional expression in Xenopus oocytes"; Ann. N.Y. Acad. Sci. 779:126-128 (1996).		
RL	COUPLING: RAPIDLY EXTRUDED FROM THE CELL DURING RELAXATION		
CC	-O-SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.		
CC	-I- ENZYME REGULATION: BY ATP.		
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.		
CC	-I- TISSUE SPECIFICITY: CARDIAC SARCOLEMMA.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@lsb-sib.ch).		
CC	EMBL: U70033; AAC46708.1; -.		
DR	MGD; MGI:10795; SLC8A1.		
DR	InterPro: IPR003644; Calx_beta.		
DR	InterPro: IPR00837; Naca_Exchanger.		
DR	InterPro: IPR004836; Na_Ca_Ex.		
DR	Pfam: PF01659; Na_Ca_Ex; 2.		
DR	Pfam: PF03160; Calx_beta; 2.		
DR	PRINTS: PRO1259; NACAEXCHNR.		
DR	SMART: SM00237; Calx_beta; 2.		
DR	TIGRFAMs: TIGR00845; caca; 1.		
KW	Transport; Antipor; Calcium transport; sodium transport; transmembrane; Glycoprotein; phosphorylation; signal; Calmodulin-binding; Gycoprotein; Phosphorylation; Signal;		
KW	SIGNAL	POTENTIAL.	
FT	CHAIN	SODIUM/CALCIUM EXCHANGER 1.	
FT	DOMAIN	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	POTENTIAL.	
FT	DOMAIN	CYTOSPLASMIC (POTENTIAL).	
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OY	593	ETVKITRKVIVDEEEYERQENFFIALEGPWKMERG-----	DR	Pfam; PF01699; Na_Ca_Ex; 2.
Db	598	EIKKTKSVKVIDEYKNTEFELGEPRIMEKKALLNLNEGGFTLTGKEMQPI	DR	pfaM; PR03160; Calx-beta; 2.
OY	628	--ISDVYDRK--LTMBEEAKRAEMKGPKVIGEHKLEVITEESY	DR	PRINTS; PR01259; NACLEXCHNGR.
Db	658	FRKVHARDHIFPSTVITISEYYDDKQPLTSKEERRIAEMGRPIGEHKLEVIOESY	DR	SMART; SM00237; Calx-beta; 2.
OY	669	EFTKTYDVLKLKTTNIALVWGTSHWDQEMERATIVSAAGDEDEDESEGERLPSCEYVMHF	DR	TIGRFAMs; TIGR00845; calca; 1.
Db	718	EFKSTWDKLKTTNIALVWGTNSWRQFQFTAATIVSAGEDDDDECGEEKLPSCFDYVMHF	DR	Transport; Airport; Calcium transport; Sodium transport;
OY	729	LTVENKVLFLACPYPPTBYCHGWCFAVSLITIGMLTAIGDLASHRGCTIGKDSVTAVFE	KW	Transport; Glycoprotein; Phosphorylation; Signal;
Db	778	LTVENKVLFLACPYPTEYNGWACTVSILMIGLLTAFICLASHRGCTIGKDSVTAVF	KW	Transmembrane; Glycoprotein; Phosphorylation; Signal;
OY	789	VAFGTSPVDPATAKAAQLDQVYADASIGNTGNSAVNVFLGLGLAWSVANIYWAQQEF	KW	Transport; Glycoprotein; Phosphorylation; Signal;
Db	838	VALGTSVPDFASKVATQDQYADASIGNTGNSAVNVFLGLGLAWSVANIYWAQQEF	KW	Transport; Glycoprotein; Phosphorylation; Signal;
OY	849	HVSAGTFLAFSVTLTFFAFYCISVLYRPPHRLGGPRCKLATWLFVSMULYL	FT	POTENTIAL.
Db	898	KVSPGTLAFSVTLTFFAFVINGVVLRYRRPEIGELGGPRKTAKLITSSLFLVLLYLIF	FT	SODIUM/CALCIUM EXCHANGER. 2.
OY	909	FATLNEYCYIKGF	FT	EXTRACELLULAR (POTENTIAL).
Db	958	: : : :	FT	CYTOSOLIC (POTENTIAL).
RESULT 9				
NAC2_HUMAN				
ID	NAC2_HUMAN	STANDARD;	PRT;	921 AA.
AC				
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein 2).			
GN	NCX2 OR KIFAA1087.			
OS	Homo sapiens (Human).			
OC	Bukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoide; Homo.			
OX	NCBI_TAXID=9606;			
RN	[1]			
RC	SEQUENCE FROM N_A.			
X	TISSUE=Brain;			
X	MEDLINE=99397452; Pubmed=10470851;			
X	Kikuno R., Nagase T., Ishikawa K.-I., Hirokawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. XIV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.", DNA Res. 6:197-205(1999).			
RA				
RT				
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RL				
CC	-I- FUNCTION: RAPIDLY TRANSPORTS Ca2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES (BY SIMILARITY).			
CC	-I- ENZYME REGULATION: BY ATP (BY SIMILARITY).			
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@ib-sib.ch).			
CC				
DR	GENERAL: AB02910; BAA83039_1; ALR_INIT.			
DR	Gene: HGNC: IHCN_1069; SLC8A2.			
DR	MM: 601901; InterPro: IPR003644; Calx-beta.			
DR	InterPro: IPR004837; NaCa_Exmem.			
DR	InterPro: IPR004836; Na_ca_Ex.			
OY	220 ILAVESPQGVQWQEGLITLFFPVCVULLAWDKRLLYKMKYRTDKHGIITETG	DB	Pfam; PF01699; Na_Ca_Ex; 2.	
Db	215 ILAVESPQGVQWQWEALITLVFVPPCVVFWAMMDKRLFYKVKYRTDRPSGIIAG	DB	pfam; PR03160; Calx-beta; 2.	
OY	160 FIAGDGPSTIVGSAFMNFIIGICWVIFDGERKIKHURFVTANMSIFAVIWL	DB	PRINTS; PR01259; NACLEXCHNGR.	
Db	155 FOAGELGPRTIVGSAFMNFIIGICWVIFDGERKIKHURFVTANMSIFAVIWL	DB	SMART; SM00237; Calx-beta; 2.	
OY	280 DHPKGEMDGKMNNSFLDGNL----VPLGEKEYDESREMIIRLKDQKHPKDLO	DB	TIGRFAMs; TIGR00845; calca; 1.	
Db	275 DPPKSTEDGTFVGAE--APGELGGLGPGPAARELDASRERVQIQLDKQKHPKDQ	DB	Transport; Airport; Calcium transport; Sodium transport;	
OY	335 LVEMANVYALSHQSKRSAYVLIQATRMMGAGNLLKKHAEQAKASSMSMVEHTPDRF	DB	Transport; Glycoprotein; Phosphorylation; Signal;	
Db	334 LVGIANYYALLHQSKRSAYVLIQATRMMGAGNLLKKHAEQAKASSMSMVEHTPDRF	DB	Transport; Glycoprotein; Phosphorylation; Signal;	
OY	395 ISKVFFDPCSYOCLENGAVLTVVRRKGDMSKTMVYDKTEDGSANAGADYEFTEGTV	DB	Transport; Glycoprotein; Phosphorylation; Signal;	

Db 393 ASIFFERSLYKILENCGSVLSSVTCOGEGNSITPYDTEGSAKGSDEYESEGTLV 452
 Qy 455 LKGETOFRPSVQIIDDIFEEDEHFEVLSNRVRIEBO---PEEMMPAFFNSLPLPR 510
 Db 453 FKGGETQELRIGTIDDDIFEEDEHFFRLNRVQDGMRQMPBPDDG-----GRPK 503
 Qy 511 AVLASPCVATVTILDHHAGIFPFECDFRHVSSEIGMEVKURTSGARGTVYPFRTVE 570
 | :
 Db 504 GRVAVPLLATVTLDDDHAGIFSQFDRLHVSCMGTVDRVRSSGARGTVRLPYRVD 563
 Qy 571 GTAKGGGFEDTYGELEFKNDTIVKTRVKIVDEEYERQENFFIALEGPWKMERGTS 630
 | :
 Db 564 GTRGGGYHYEDAGELEFGDDTMKTLQKVIVDVEEYKONFFILQGPQWLKGISA 623
 Qy 631 VT-----DRKLIMEEAKRATIEMKGKVVLGERPKLEVIESEYYEFKTVDKLKKNL 684
 Db 624 LLIQNGGDGDRKLAAEERARRAEMGKVVLGERPKLEVIESEYYEFKTVDKLKKNL 683
 Qy 685 LVVGTHSRDQFMEAITYSAACDDEDESG--ERLPLSCFDYWMELTVFMWVLFACVPP 742
 | :
 Db 684 LVGTHSWRQEFLAEITVS-ASGDEEEEDGSRERLPLSCFDYWMELTVFMWVLFACVPP 742
 Qy 743 TECHGHWACFAVSIILQMLTAIGDLASHGGTIGKDSVTAVVEAAGFTSPUDTFASK 802
 | :
 Db 743 TECHGHWACFGYSILVILQLTALIGDLASHGGTIGKDSVTAVVEAAGFTSPUDTFASK 802
 Qy 803 AAHQDVADASIGNVTSNAVNVLGLANSVAATWALOGQEFWVSGAIIASFSTLF 862
 | :
 Db 803 VAHQDVADASIGNVTSNAVNVLGLANSVAATWALOGQEFWVSGAIIASFSTLF 862
 Qy 863 TTFAVFCISVLLRRPHGGPQQCKLATWLFVSLWLYILFATELYCYIKGF 921
 | :
 Db 863 TVFVFVGLAVLRRPHGGPQQCKLATWLFVSLWLYILFASLEACHIRGF 921
 RESULT 10
 NAC2_RAT STANDARD: PRT: 921 AA.
 AC P48768;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 13-JUN-2002 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein 2).
 DE SLC8A2 OR NCX2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TAXID:10116;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain stem;
 RX MEDLINE=9429496; PubMed=8021246;
 RA Li Z., Matsuo S., Hryshko L.V., Nicoll D.A., Bershon M.M.,
 RA Burke E.P., Lifton R.P., Philippou K.D.;
 RT "Cloning of the NCX2 isoform of the plasma membrane Na(+) -Ca2+
 exchanger.",
 J. Biol. Chem. 269:17434-17439(1994).
 RN [2]
 RP TISSUE SPECIFICITY.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=9638463; PubMed=8798769;
 RA Nicoll D.A., Oudehau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
 RA Phillipson K.D.;
 RT "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.",
 J. Biol. Chem. 271:24914-24921(1996).
 CC -1- FUNCTION: RAPIDLY EXTRUDED FROM THE CELL DURING RELAXATION
 COUPLING. Ca2+ IS EXTRUDED FROM THE CELL DURING RELAXATION
 SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
 CC -1- ENZYME REGULATION: BY ATP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: BRAIN AND SKELETAL MUSCLE.

CC -----
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 CC -----
 DR InterPro: IPR04336; Na_Ca_Ex.
 DR PRO1699; Na_Ca_Ex.
 DR PF03160; Calx-beta.
 DR PRINTS: PRO1259; NACAEXCHNR.
 DR SMART: SM0237; Calx-beta.
 DR TIGRFAM; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Glycoprotein; Phosphorylation; Signal;
 KW Calcium membrane; Glycoprotein; phosphoylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 21 921 68 20
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QY	206 TAAMSIFAYWLYMLILAVFSPGVVQVWEGLITLEFFPVCVLLAWADKRLIIFYKMHKKY 265
CC	TO PREVENT OVERLOADING OF INTRACELLULAR STORES (BY SIMILARITY).
CC	-! ENZYME REGULATION: BY INTRACELLULAR CALCIUM IONS (BY SIMILARITY).
CC	-! SUBCELLULAR LOCATION: Integral membrane protein.
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CC	-----
Db	KDLKQHKPEKDQLQVEMANYALSHQQSKAFYRQATRTAGNGLKKHAEQAKKA 380
QY	321 KDLKQHKPEKDQLQVEMANYALSHQQSKAFYRQATRTAGNGLKKHAEQAKKA 380
Db	RTDKHGIETEGDHPKGKEMDGKMMNSHFLDGNL---VPLSCKEVDSREMRTRL 320
QY	320 KDLKQHKPDQLEOLVGIAKYALHQQSKAFYRQATRTAGNGLKKHAEQAKKA 379
Db	RTDPGSGIIGAEGDPKSKEBLDGTVGTE VPGEIGALGTGPAEARLDAEASREVYQIL 319
QY	381 SSMEVHTDSEDFTSKVFTPCSTYOCLENGSVLISVALQEGEGNSTFYDRTEDGA 440
Db	380 GA-NDGAPDDEDDGASRIFEFPSLYHCLENGGSVLSVALQEGEGNSTFYDRTEDGA 438
QY	441 NAGADEYFTGTVWKLKPGEQKEFSGVIIIDIFEDDEHFFVRLSNVRIEEQ---PEE 496
Db	441 NAGADEYFTGTVWKLKPGEQKEFSGVIIIDIFEDDEHFFVRLSNVRIEEQ---PEE 496
QY	439 KAGSDYEYSCTLVKPGETOKERLIGITDIFEDDEHFFVRLSNVRIEEQ---PEE 498
Db	439 KAGSDYEYSCTLVKPGETOKERLIGITDIFEDDEHFFVRLSNVRIEEQ---PEE 498
OY	497 GMPPATFNSPLPRAVLASPCVATVILDDHAGTFECDTIHSESGMNEVKLRTS 556
Db	499 G-----GRPKERLVAAPLATVILDDHAGTFECDTIHSESGMNEVKLRTS 549
QY	557 GARGTVIPPTVEGTAKGGEDFEDTYGIELEFKNDETVKTRVKTDEREVYERONIFT 616
Db	550 GARGTVIPPTVEGTAKGGEDFEDTYGIELEFKNDETVKTRVKTDEREVYERONIFT 609
QY	617 ALGERKWWMERGISDYM----DRKTJMEEEAKRAEMGKPVGHLKPVVILIESYF 670
Db	617 ALGERKWWMERGISDYM----DRKTJMEEEAKRAEMGKPVGHLKPVVILIESYF 616
Db	ELGQDPOWLKRQKISALLNQGDCDKTAAEQAIRAEQMNGCPLVGLNCRLVIEESYD 669
OY	671 KTVDKLIKINTLNALWGTSHWDQMEALTVSAQDEDDES - EERLPSCDFVMHF 728
Db	670 KTVDKLIKINTLNALWGTSHWDQMEALTVSAQDEDDES - EERLPSCDFVMHF 728
QY	729 LTVENKVLFCACVPPTEXCHOMACFAVSILIGMLTAIGDLASHECTIGLKDSVAVFE 788
Db	729 LTVENKVLFCACVPPTEXCHOMACFAVSILIGMLTAIGDLASHECTIGLKDSVAVFE 788
QY	789 VAFGTSVPDTFASKAALQWYADASIGNTGSNAVNFGIGLAMSVAIYWAQOEF 848
Db	789 VAFGTSVPDTFASKAALQWYADASIGNTGSNAVNFGIGLAMSVAIYWAQOEF 848
Db	VALGTSVPDTFASKAALQWYADASIGNTGSNAVNFGIGLAMSVAIYWAQOEF 848
OY	849 HVSAGTLAFSTVLFTIFAFICISVLRYRRPHLGGLGPCKLATTWFLVSLWLYL 908
Db	849 EVRTGTLAFSTVLFTIFAFICISVLRYRRPHLGGLGPCKLATTWFLVSLWLYL 908
QY	909 FATELEYCYTRGF 921
Db	909 FASLENYCHTRGF 921
RESULT 11	
NAC3_HUMAN	
ID	NAC3_HUMAN STANDARD; PRT; 595 AA.
AC	P57103; 16-Oct-2001 (Rel. 40, Created)
DT	16-Oct-2001 (Rel. 40, Last sequence update)
DT	15-Jun-2002 (Rel. 41, Last annotation update)
DE	Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein 3) (Fragment).
DE	SLC8A3 OR NCX3.
OS	Homo sapiens (Human).
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
OX	NCBI_TAXON=9605;
[1]	SEQUENCE FROM N. A.
RP	Kraev A.S., Chumakov I.M., Carafoli E.;
RT	"The organization of the human gene of the sodium-calcium exchanger.";
RT	Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
-! FUNCTION: RAPIDLY TRANSPORTS Ca2+ DURING EXCITATION-CONTRACTION	
QY	361 MMTGAGNTIKKHAEQKASSMEVHEDPEPFSKVFEDCSYQLENGCAVLTWVR 420
Db	361 MMTGAGNTIKKHAEQKASSMEVHEDPEPFSKVFEDCSYQLENGCAVLTWVR 420
QY	301 LPVLEGKDEVDESREMIRLKDQKHKPEKDQLQVEMANYALSHQQSKAFYRQATR 360
Db	301 LPVLEGKDEVDESREMIRLKDQKHKPEKDQLQVEMANYALSHQQSKAFYRQATR 360
QY	241 FPPCVLLAWADKRLFVKYMHKKYRDHKRGITETGDHPKGLEMCGKMMNSHFLDG 300
Db	241 FPPCVLLAWADKRLFVKYMHKKYRDHKRGITETGDHPKGLEMCGKMMNSHFLDG 300
QY	181 IIGCIVVYIPDGTRKHLRVEFTIAWSIAFYIWLMLAVFSPGVVQWEGLTLUFF 240
Db	181 IIGCIVVYIPDGTRKHLRVEFTIAWSIAFYIWLMLAVFSPGVVQWEGLTLUFF 240
QY	121 TSIWTPTRVNETWSNLTLMALGESSAPPELTSLLSIEVCGFIAQDGGPSTVGSAAFNFT 180
Db	121 TSIWTPTRVNETWSNLTLMALGESSAPPELTSLLSIEVCGFIAQDGGPSTVGSAAFNFT 180
QY	61 PIWPPENPSLGDKIAKRVVYVALIYMLGLGVSTIADRMASIEVITSOREVTKKPNGE 120
Db	61 PIWPPENPSLGDKIAKRVVYVALIYMLGLGVSTIADRMASIEVITSOREVTKKPNGE 120
QY	121 TSIWTPTRVNETWSNLTLMALGESSAPPELTSLLSIEVCGFIAQDGGPSTVGSAAFNFT 180
Db	121 TSIWTPTRVNETWSNLTLMALGESSAPPELTSLLSIEVCGFIAQDGGPSTVGSAAFNFT 180
QY	181 IIGCIVVYIPDGTRKHLRVEFTIAWSIAFYIWLMLAVFSPGVVQWEGLTLUFF 240
Db	181 IIGCIVVYIPDGTRKHLRVEFTIAWSIAFYIWLMLAVFSPGVVQWEGLTLUFF 240
QY	121 TSIWTPTRVNETWSNLTLMALGESSAPPELTSLLSIEVCGFIAQDGGPSTVGSAAFNFT 180
Db	121 TSIWTPTRVNETWSNLTLMALGESSAPPELTSLLSIEVCGFIAQDGGPSTVGSAAFNFT 180
QY	301 LPVLEGKDEVDESREMIRLKDQKHKPEKDQLQVEMANYALSHQQSKAFYRQATR 360
Db	301 LPVLEGKDEVDESREMIRLKDQKHKPEKDQLQVEMANYALSHQQSKAFYRQATR 360

OY	421 KGGDSKTMVYDVKTEGDSANAGADEFTEGTVLKGTEOKFSVGIDDDIFEEHF	DR	Interpro; IPR004837; NaCa_Exemb.
		Pfam;	PF01699; Na_Ca_Ex; 3.
Db	421 KGGDSKTMVYDVKTEGDSANAGADEFTEGTVLKGTEOKFSVGIDDDIFEEHF	DR	TIGRFAMS; TIGR00367; K_Nacaexchang-rel; 1.
OY	481 FVRLSNVRIEREQEPMMPAIFNSLPLPRAVLSPASCATVATILDDHAGFTFEDTH	KW	Vision; Transport; Antiport; Symport; Calcium transport; Potassium transport; Transmembrane; Glycoprotein;
Db	481 FVRLSNVRIEREQEPMMPAIFNSLPLPRAVLSPASCATVATILDDHAGFTFEDTH 540	KW	Potassium transport; Transmembrane; Glycoprotein;
OY	541 VSEISIGMEVKLRTSGARGTVIPVRTVECTAKSGGEDFEDTYGLEFKIDTV 595	KW	Phosphorylation; Signal; Repeat; Alternative splicing.
Db	541 VSEISIGMEVKLRTSGARGTVIPVRTVECTAKSGGEDFEDTYGLEFKIDTV 595	FT	SIGNAL 1 38
GN	SLC24A1 OR NCKX1	FT	CHAIN 39 1216
OS	Bos taurus (Bovine).	FT	DOMAIN 39 446
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.	FT	TRANSMEM 447 467
OC	NCBI_TaxId:9913;	FT	DOMAIN 468 491
RN	[1] SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 66-88; 232-249; RP 647-660 AND 1119-1136.	FT	TRANSMEM 492 512
RC	TISSUE=Retina;	FT	DOMAIN 513 518
RX	Medline=92258377; Pubmed=1582405;	FT	TRANSMEM 519 539
RA	Reilaender H., Achilles A., Friedel U., Maul G., Lottspeich F., RA Cook N.J.;	FT	TRANSMEM 540 557
RA	"primary structure and functional expression of the Na/Ca, K-exchanger from bovine rod photoreceptors.";	FT	TRANSMEM 558 578
RL	EMBO J. 11:1689-1695(1992).	FT	TRANSMEM 1046 1052
RN	[2] SEQUENCE OF 725-1216 FROM N.A. (ISOFORM 1).	FT	TRANSMEM 1053 1073
RC	TISSUE=Retina;	FT	TRANSMEM 1074 1088
RX	Medline=98138491; Pubmed=9478004;	FT	TRANSMEM 1089 1109
RA	Tucker J.E., Winkfein R.J., Cooper C.B., Schnettkamp P.P.M.;	FT	TRANSMEM 1110 1127
RT	"cDNA cloning of the human retinal rod Na Ca+K exchanger: comparison with a revised bovine sequence.";	FT	TRANSMEM 1128 1148
RL	Invest. Ophthalmol. Vis. Sci. 39:435-440(1998).	FT	TRANSMEM 1149 1157
CC	- FUNCTION: Critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Light causes a rapid lowering of cytosolic free calcium in the outer segment of both retinal rod and cone photoreceptors and the light-induced lowering of calcium is caused by extraction via this protein which plays a key role in the process of light adaptation. Transports one Ca(2+) and one K(+) in exchange for four Na(+). (By similarity).	FT	TRANSMEM 1158 1178
CC	- SUBCELLULAR LOCATION: Integral membrane protein.	FT	TRANSMEM 1179 1185
CC	- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.	FT	TRANSMEM 1186 1206
CC	- TISSUE SPECIFICITY: Retina.	FT	TRANSMEM 1207 1216
CC	- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.	FT	TRANSMEM 1296 1298
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	FT	TRANSMEM 1303 1303
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Db	596	WNQOLBLWVKEQLNKRPAKKMAGLDSLKPQDGTVVDEQODNNKKLQLSSMLTRG---S	51	RL	An. J. Physiol.	278:C651-C660(2000).
Qy	300	NLVPLEGKEYEDSER-E-MIRILDKQKHEPKDQ--LVEMANYALSHQQSKAFYI	356	RN	[12]	SEQUENCE OF 1067-1155 FROM N.A.
Db	652	SSASLHNSTIRSTIVQLMLHSIDPLGEARPSKDKBEETLYPEAK	695	RP	White K.E., Gesek F.A., Friedman P.A.;	
Qy	357	QATRMTAGNGLKKHAEQAKKASSMSEVHTDDEP-----DFISKVFEDPCSYQC	407	RL	Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.	
Db	696	-----ATPQKAESKPEEPKALPEVTVPAPADVKGLOEEDPGSQV	739	CC	-1- FUNCTION: Critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Light causes a rapid lowering of cytosolic free calcium in the outer segment of both retinal rod and cone photoreceptors and the light-induced lowering of calcium is caused by extrusion via this protein which plays a key role in the process of light adaptation. Transports one Ca(2+) and one K(+) in exchange for four Na(+).	
Qy	408	--LENCG-----AVLTIVRKGGDMKTMVVDYKTEDGS----ANAGADYEFT	449	CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.	
Db	740	GAEAENTGERTGGEREAPACGEGENGERSGGDAALGGESEGKAENESEGDIPARRGIDE-D	798	CC	-1- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here) 2, 3 and 4; are produced by alternative splicing.	
Qy	450	EGTVVLKPGTETOKERSVGT-----DDTIE-----EDEHFFVRLNV	487	CC	-1- TISSUE SPECIFICITY: Highly expressed in the eye.	
Db	799	EGEIGAEGGEVKGDEDEGEIQAGEEGEGEVEGDEDEGEIQAGEAG	858	CC	-1- SIMILARITY: BELONGS TO THE SLC2A FAMILY OF TRANSPORTERS.	
Qy	488	RIEEOPE-----EGMPATFNSIPLPRAVLASPVCATVILDDDHAGIFTFEC	536	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@ib-sib.ch).	
Db	859	EVEGEGDEGEIQAGEEGEVG-----DEDEGEIQAGEA	891	CC	INTERPRO: IPR004481; K_NaCaexchange.	
Qy	537	DTIHVSEISIGMEVKVLRITSGARGTVIPVRTVECTAKGG----GEDFDTGELEFK	590	CC	INTERPRO: IPR004837; NaCa_Ex; 3.	
Db	892	GEVEGEDEDEGEIQ-----AGEGEGEV-----KGDEGEIQAGEAGEVED	936	CC	TIGRFAMS: TIGR00367; K_NaCaexchange-rel; 1.	
Qy	591	NDETVKTIRKVIRKDVREYERQENFETALGPKWMERGI-----SDVYDRKLMEEEE	642	CC	EMBL: AF176688; AAD53121.1; -.	
Db	937	EDE--GEIQAGEEGEGETGEQEELNAEIOGEAKDDEEGDGGDGSDEEDEEEEEE	944	CC	EMBL: U49253; AAB37753.1; -.	
Qy	643	AKRIAMKGKPVGLERPKLEVIEEYEFKITVVDKLKIKTNALAVGTHSWRDQFMEATV	702	CC	INTERPRO: IPR004817; K_NaCaexchange.	
Db	995	D-----EEEEE-----EEEEE-----	1000	CC	INTERPRO: IPR004837; NaCa_Ex; 3.	
Qy	703	SAAGDEDEDESGEERLPSCDFY-----VMHFLTVFWKVLFACVPPTECHGWCFAV	754	CC	TIGRFAMS: TIGR00927; ZA1004; 1.	
Db	1001	--BEEEEEENQPLSLEWPERRRKQAIYFLFLPIVPLWLTVPDVRLEAKKFV	1056	CC	VISION: Transport; Antipor; Symport; Calcium transport; Repeat; Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat; Alternative splicing.	
Qy	755	--SILIGMTATIGDLASHFGCTIGLDSVTAVFVGFTSPDTEASKAAQDYY	810	CC	KW POTENTIAL.	
Db	1057	TFLGSILWILWAMPYLMWWAHQVGETIGLSISEIMGLTILAGTSIDLITSVIARKGL-	1115	CC	FT SIGNAL 1 38 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.	
Qy	811	ADASIGNVIGNSNAVNVFLGIGLAWMSVAITKWLQOEFHVSAGTAFAFSVNLFTIFAFVCI	870	CC	FT DOMAIN 39 1181 EXTRACELLULAR (POTENTIAL).	
Db	1116	GDMAYSSVSNIFDITVGLPPLWFLSILINGLOPVAWS-SNLGFCIAIVLFLMFVIS	1174	CC	FT DOMAIN 40 419 CYTOPLASMIC (POTENTIAL).	
Qy	871	SVLLYRRRPHLGEGLGGPRGCKLATW-----LFWSLWLXLYLF 909	1175	CC	FT DOMAIN 41 464 EXTRACELLULAR (POTENTIAL).	
Db	1175	SIAL-----CK---WRMWKILGETMFILYVF	1198	CC	FT DOMAIN 42 465 EXTRACELLULAR (POTENTIAL).	
RESULT 13						
N _X 1_RAT	STANDARD;	PRT;	1181 AA.	FT DOMAIN 43 485 EXTRACELLULAR (POTENTIAL).		
AC Q9ZQ66; 062932;				FT DOMAIN 44 512 EXTRACELLULAR (POTENTIAL).		
DT 15-JUN-2002 (Rel. 41, Created)				FT DOMAIN 45 519 EXTRACELLULAR (POTENTIAL).		
DT 15-JUN-2002 (Rel. 41, Last sequence update)				FT DOMAIN 46 544 EXTRACELLULAR (POTENTIAL).		
DE 15-JUN-2002 (Rel. 41, Last annotation update)				FT DOMAIN 47 552 EXTRACELLULAR (POTENTIAL).		
DE sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-exchange protein 1) (Retinal rod Na+Ca+K exchanger);				FT DOMAIN 48 569 EXTRACELLULAR (POTENTIAL).		
DE exchange protein 1 (Retinal rod Na+Ca+K exchanger);				FT DOMAIN 49 570 EXTRACELLULAR (POTENTIAL).		
GN SLC2A1 OR NCKX1.				FT DOMAIN 50 989 EXTRACELLULAR (POTENTIAL).		
OS Rattus norvegicus (Rat).				FT DOMAIN 51 1010 EXTRACELLULAR (POTENTIAL).		
OC Bivalvia; Chordata; Craniata; Vertebrata; Euteleostomi;				FT DOMAIN 52 1017 EXTRACELLULAR (POTENTIAL).		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				FT DOMAIN 53 1038 EXTRACELLULAR (POTENTIAL).		
NCBI_TAXID=10116;				FT DOMAIN 54 1039 EXTRACELLULAR (POTENTIAL).		
RN [1]				FT DOMAIN 55 1074 EXTRACELLULAR (POTENTIAL).		
RP SEQUENCE FROM N.A.' AND ALTERNATIVE SPlicing.				FT DOMAIN 56 1075 EXTRACELLULAR (POTENTIAL).		
RC STRAIN-Sprague-Dawley; TISSUE-Eye;				FT DOMAIN 57 1092 EXTRACELLULAR (POTENTIAL).		
RX MEDLINE=20217352; PubMed=10751314;				FT DOMAIN 58 1103 EXTRACELLULAR (POTENTIAL).		
RA Lyon S., Leach S., Li X.-F., Tucker J.E., Schnetkamp P.P.M.,				FT DOMAIN 59 1113 EXTRACELLULAR (POTENTIAL).		
RA Lytton J.;				FT DOMAIN 60 1114 EXTRACELLULAR (POTENTIAL).		
RT "Alternatively spliced isoforms of the rat eye sodium/calcium-potassium exchanger NCKX1.";				FT DOMAIN 61 1121 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 62 1142 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 63 1143 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 64 1150 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 65 1171 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 66 1172 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 67 1181 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 68 461 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 69 501 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 70 1061 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 71 1092 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 72 730 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 73 741 EXTRACELLULAR (POTENTIAL).		
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RT				FT DOMAIN 77 791 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 78 792 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 79 804 EXTRACELLULAR (POTENTIAL).		
RT				FT DOMAIN 80 817 EXTRACELLULAR (POTENTIAL).		

REPEAT	818	830	8.	
FT REPEAT	831	843	9.	
FT REPEAT	844	856	10.	
FT REPEAT	857	869	11.	
FT REPEAT	870	881	12.	
FT REPEAT	882	893	13.	
FT REPEAT	894	905	14.	
FT DOMAIN	952	974	POLY-GLU.	
FT MOD-RES	625	625	PHOSPHORYLATION (POTENTIAL).	
FT CARBOHYD	271	271	N-LINED (GLCNAC -) (POTENTIAL).	
FT VARSPLIC	598	710	MISSING (IN ISOFORM 2).	
FT VARSPLIC	616	710	MISSING (IN ISOFORM 3).	
FT VARSPLIC	652	679	MISSING (IN ISOFORM 4).	
SQ SEQUENCE	1181 AA;	12980 MW;	B063C1C1193696AE CRC64;	
Query Match	6.3%	Score 303.5; DB 1; Length 1181;		
Best Local Similarity	20.4%	Pred. No. 5.3e-12; Matches 194; Conservative 131; Mismatches 305; Indels 321; Gaps 40;		
Qy	77	VIVVFVALLMFLGVSIAADR-FMASIEVITSQEREVITKKPGETSTTIRVNETVN 135		
Qy	422	VVLHIFGMGVFVVALAIVCPEYFVPLAGVTD-----LOI-SEDVAG 463		
Qy	136	UTLMALGSSAPEILSLLIEVCGHGTIA-GDLGPSTIVGSAFAFNMFIIIGCYYVPDGET 194		
Db	464	ATFMAGGSAPELFLSLIGH----FISHNIVGIGITIVGSAVNFILFVIGCALF----S 514		
Qy	195	RKIKHLRVEFITAAMSIFAYIWLY----NIALVEFSPGVVWVNGLITFFFPVCV--- 245		
Db	515	REILNL-----TWWPLFRUVSFYILDLSMLIVFLDSLAWWSLLLLAYALVYFTMK 568		
Qy	246	---LLAWVADK--RLFVYKMHKVKRTDKHRKGIIETECDHPKGEM-----DSK 290		
Db	569	WNKOERWRVKEQLRSRRPVKAVALGMDLSKSDGAEEENSCQDNKIKLPLSSVLTGRGSSAS 628		
Qy	291	MNNS -----HFLDGNLYPL---EGKDEESREMIRILDKL-----QKH----- 328		
Db	629	LHNSLIRSTTYLHMJHSUDLGGEARPSKKQKQESLNQEARVLPQTAKESSSDEEPRAELPA 688		
Qy	329	-----EKDQLQVEMANYVALSHQOKSRAFYRTOATRMTGAGN 367		
Db	689	WTWTPAPAPDKQDQEEDPCQCEDVDEAEHRGDMTGEGERESEA---EGKDEEGETE 744		
Qy	368	ILKKHAAEQKKKASSMSEVITDEPDFISKVFFDPSCSYQCOLENGAVAILTVRKGGDMSK 427		
Db	745	AERKEDQEEBETETKGKEKEGETES-----EGKDK--- 774		
Qy	428	TWIVDKYKTGDSANAGADYE---FTEGVVLKPGTOKERSVGIIDDDIFFE----- 475		
Qy	476	-----EDEHFVURLSNRVTEEEQPT--ECMPAFLNSFLPLPRAVLASPVCATV 522		
Db	828	QEGETEAEGEKEVER-----EVETBAERKETNHEGETEREGK----- 863		
Qy	523	ILDDDHAGHTEFECTDTHESIGMEVKVLTSGARGTVVPPRTVEGTAKGGDED 582		
Qy	864	--EADREGETEAEGEVEHOGE-----TEAEKV----EHEGETEAGEKEHE 904		
Qy	583	TYGELEFKNDNEVKIRVIVD---EEEERQENFIAGPKMMERGSSDVDRKLME 639		
Qy	905	--GOSETQADT-----EVKDGGGEAEANAEDOCETAGEGKGADGGGGSDGSEEEED 956		
Db	968	-----EEEEESEEE--PLSLEMPESIQRQQAIALYFLPFLIPWLWTPDVROEARKF 1018		
Db	957	EEDEEE-----EEEEE----- 967		
Qy	700	ITVSAGGDDDEDEGEERIFSCFV-----VMHLLVFWKLFACVPPTECHGMAC 751		
Qy	640	EEAKRIAENKGKPVLGEHPKLEVITEESVFKTTVDKLIRKTNLALVVGTHSWRDQFMEA 699		
Qy	752	FAV----SLLIGMTAIIGLASHFGCTIGLKDSVTAVVFAFGTSVPTDFASKAALQ 807		
Db	1136	FVIFS-----ASCK---WMNKTLGETMFLLYFVFLV 1166		
Db	1019	FVTELGSIWIAMIAMSFLYWAHQWTGIGISEEIMGLTAACTGTTPLTSVARK 1078		
Db	808	DYVADISIGNVTGSNAVNVLGIGLAWSAVAYWALOGOFHVA-GTIAFSVLTIF 866		
Qy	1079	GL-GDMAVSSSVGSNFDITVGLPVFWLFLSLLNAL-QPIVSSNGLFCIAVLFMLL 1135		
Qy	867	FVCSISLYRRPHIGEGLGGPRGCKLAW---LFVSLWLLILFATL 912		
RESULT 14				
NKX1_HUMAN				
ID				
060721; O43485; 075184;				
AC				
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-exchange Protein 1) Retinal rod Na-Ca+K exchanger).			
DE	SLC2A1 OR NCKX1 OR KIAA0702.			
GN				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Nammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.			
OC				
OX				
RN	[1] NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Retina;			
RC	LINE=9072302; PubMed=9856482;			
RA	Tucker J.E., Winkfein R.J., Murthy S.K., Friedman J.S., Walter M.A., Demerick D.J., Schnetkamp P.P.M.,			
RA	"Chromosomal localization and genomic organization of the human retinal rod Na+Ca+K exchanger";			
RT	retinal rod Na+Ca+K exchanger;			
RT	Hum. Genet. 103:411-414(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Retina;			
RC	LINE=93138491; PubMed=9478004;			
RC	Tissue=Brain;			
RC	LINE=98403880; PubMed=9734811;			
RA	Ishikawa K.-I., Nagase T., Syama M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,			
RA	"Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.,"			
RA	DNA Res. 5:169-176(1998).			
CC	-- FUNCTION: Critical component of the visual transduction cascade, controlling the calcium concentration of outer segments during light and darkness. Light causes a rapid lowering of cytosolic free calcium in the outer segment of both retinal rod and cone photoreceptors and the light-induced lowering of calcium is caused by extrusion via this protein which plays a key role in the process of light adaptation. Transports one Ca(2+) and one K(+) in exchange for four Na(+)."			
CC	-- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.			
CC	-- TISSUE SPECIFICITY: Found only in the outer segments of retinal rod photoreceptors.			
CC	-- SIMILARITY: BELONGS TO THE SLC2A FAMILY OF TRANSPORTERS.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation in the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/			

CC or send an email to license@lsb-sib.ch).

Db	614 -LSRRPVKWAEDL---SKPGDGA-----AVDEIQDNK--KUKLPSLT---	654
Qy	368 ILKKHAAEQAKKASSEWHTDEPDFISKVF--FDPCSYQCLENCGRVLLTVRKGGD	424
Db	655 -----RGSSSTSLNSTIRSTYQIOLMHSIDP-----LREVR---	686
DR	EMBL: AF062921; AAC16732; 1; -	
DR	EMBL: AF062922; AAC17912; 1; -	
DR	EMBL: AF05132; AAB97832; 1; -	
DR	EMBL: AB04602; BA31677; 1; ALT_SEQ.	
DR	GeneID: HGNC:10975; SLC24A1.	
DR	MIM: 603617; -.	
DR	InterPro: IPR004817; K_NaCaexchang.	
DR	InterPro: IPR00481; K_NaCaexchang.	
DR	InterPro: IPR004837; NaCa_Exemb.	
DR	Pfam: PF01699; Na_Ex_3.	
DR	TIGR4MS; TIGR0367; K_NaCaexchang-re1; 1.	
DR	TIGR4MS; TIGR00927; 2A1904; 1.	
KW	Transport; Antiport; Symport; Calcium transport;	
KW	Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;	
KW	Alternative splicing.	
FT	SIGNAL 1 38	
FT	CHAIN 39 1099	
FT	DOMAIN 39 452	
FT	TRANSMEM 453 473	
FT	DOMAIN 474 497	
FT	TRANSMEM 498 518	
FT	DOMAIN 519 522	
FT	TRANSMEM 523 543	
FT	DOMAIN 544 563	
FT	TRANSMEM 564 584	
FT	DOMAIN 585 585	
FT	TRANSMEM 586 606	
FT	DOMAIN 607 907	
FT	TRANSMEM 908 928	
FT	DOMAIN 929 935	
FT	TRANSMEM 936 956	
FT	DOMAIN 957 971	
FT	TRANSMEM 972 992	
FT	DOMAIN 993 1010	
FT	TRANSMEM 1011 1031	
FT	DOMAIN 1032 1039	
FT	TRANSMEM 1040 1060	
FT	DOMAIN 1061 1068	
FT	TRANSMEM 1069 1089	
FT	DOMAIN 1090 1099	
FT	REPEAT 494 534	
FT	REPEAT 979 1010	
FT	DOMAIN 860 890	
FT	MOD_RES 658 658	
FT	CARBONYL 290 290	
FT	VARSPC 631 648	
FT	CONFLICT 516 516	
FT	SEQUENCE 1099 AA: 121374 MN: 3911856BB08B5FD CRC64:	
Query Match	6.1%; Score 293; DB 1; length 1099;	
Best Local Similarity	21.7%; Pred. No. 2.4e-11; Matches 191; Conservative 122; Mismatches 268; Indels 298; Gaps 42;	
Matches	191; Conserve 122; Mismatches 268; Indels 298; Gaps 42;	
RESULT 15		
NKX3_MOUSE	ID NKX3_MOUSE STANDARD; PRT: 645 AA.	
AC	Q99PD7; Q99PD8; Q99JR2;	
DT	15-JUN-2002 (Rel. 41, Last sequence update)	
DT	15-JUN-2002 (Rel. 41, Last annotation update)	
DE	Sodium/potassium/calcium exchanger 3 precursor (Na(+)/K(+)/Ca(2+)-exchange protein 3).	
GN	SLC24A3 OR NCX3.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Butheroidea; Rodentia; Sciurognathii; Muridae; Murinae; Mus.	
RN	[1] NCBL_TaxID=1090;	
RP	SEQUENCE FROM N.A.	
RC	RC STRAIN=129/SVJ and CD-1; TISSUE=Embryonic stem cells, and Brain;	
RK	MEDLINE=21303617; PubMed=11294880;	
RK	Kraev A., Quedau B., Leach S., Li X.-F., Dong H., Winkfein R.,	
RK	Perizzolo M., Cai X., Yang R., Phillipson K.D., Lyton J.;	
RK	"Molecular cloning of a third member of the potassium-dependent	
RT	sodium-calcium exchanger gene family, NCX3;"	
RL	J. Biol. Chem. 276:23161-23172 (2001).	
RN	[2] SEQUENCE OF 323-645 FROM N.A.	
RP	TISSUE=Breast tumor;	
RC	Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.	
CC	- FUNCTION: Transports one Ca(2+) and one K(+) in exchange for four Na(+) (By similarity).	

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Abundant in the brain. Highest levels found in
 CC selected thalamic nuclei, hippocampal CA1 neurons and in layer IV
 CC of the cerebral cortex.
 CC -!- SIMILARITY: BELONGS TO THE SLC2A FAMILY OF TRANSPORTERS.

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CC DR EMBL; AP314821; AAG60049.1; -
 CC DR EMBL; BC0314822; AAG60050.1; -
 CC DR EMBL; BC005472; AAG60542.1; -
 CC DR MGD; MGJ:2137513; SLC2A3.
 DR InterPro; IPR004481; K_NaCexchng.
 DR InterPro; IPR004837; NaCa_Ex; 3.
 DR Pfam; PF01695; Na,Ca_Ex; 3.
 DR TIGRFAMS; TIGR00367; K_NaCexchng-rel; 1.
 DR Transport; Antiport; Symport; Calcium transport; Potassium transport;
 Sodium transport; Transmembrane; Glycoprotein; Signal; Repeat.
 KW SIGNAL 1 : 43
 FT CHAIN 44 : 645
 FT DOMAIN 44 : 106
 FT TRANSMEM 107 : 127
 FT DOMAIN 128 : 151
 FT TRANSMEM 152 : 172
 FT DOMAIN 173 : 181
 FT TRANSMEM 182 : 202
 FT DOMAIN 203 : 209
 FT TRANSMEM 210 : 230
 FT DOMAIN 231 : 234
 FT TRANSMEM 235 : 255
 FT DOMAIN 256 : 486
 FT TRANSMEM 487 : 507
 FT DOMAIN 508 : 512
 FT TRANSMEM 513 : 533
 FT DOMAIN 534 : 551
 FT TRANSMEM 552 : 572
 FT DOMAIN 573 : 582
 FT TRANSMEM 583 : 603
 FT DOMAIN 604 : 617
 FT TRANSMEM 618 : 638
 FT DOMAIN 639 : 645
 FT TRANSMEM 645 : 188
 FT REPEAT 520 : 551
 FT DOMAIN 424 : 430
 FT CARBOHD 70 : 85
 SO SEQUENCE 645 AA; 71914 MW; C62DBE6CBA01C96 CRC64;

Query Match 5.5%; Score 266; DB 1; Length 645;
 Best Local Similarity 19.1%; Pred. No. 6.6e-10;
 Matches 162; Conservative 94; Mismatches 216; Indels 374; Gaps 30;

Qy 77 VIVYFVALIYMFGLGVSIADR-FMASLEVTISQEREVTVKPNGETSTITIRWNNETVSN 135
 Db 109 VVHLVLCAMYMFYALATVCDDFVPSLKEKICERLH-----:|: LSEBVAG 150
 Qy 136 LTIMALGSSAPEPLLSSLIEVGCHGFFIA-GDILGPSTIVGSAAFNMFIIGICVVYVIPGET 194
 Db 151 ATPEMAAGSSAPELFSTVIGV---FITKGDVGVGTIVGSAVNLIICLIGVGLFA-GQV 204
 Qy 195 RKKHLRVEFTIAW---SFAYTIVMLMIAVESPQVWVREGULITLEFPVCVLLAW 249
 Db 205 VAL-----SSWCLLRDSTIYTISVVALVIFIDEKVSWESLVLVLMYLIVI- 253
 Qy 250 VADKRLFLFYKVMMKKYKPDKHGGILITEGDPHKG-LMDGMMSNSHLDGNLNUPLGKEV 309
 Db 254 -----MKYNACIHOQCFERTTKG-----AGNNNG--LANN----AEI 284

Qy 310 DESRREMTRILKDKOKHPEKDQLDOLVEMANYALSHQQSKSRAFYRQATRMGTAGNLT 369
 Db 285 DDS----- 287
 Qy 370 KKHAEQAKKASSMSEYHTDEPEDFTSKVFDPGCSYQCLENGAVLITVVRGGDSKTM 429
 Db 288 -----SNCDATV----- 294
 Qy 430 YVDYKTEDSANAGADTEFFECTIVLKPGEOFKEFSVGIODDIFEEDEHFVRLSVNR 489
 Db 295 -----VLRKKAENFURKASTIMVNB-----LUSAYPH 320
 Qy 490 EEEQPECOPPAIFNSLPLPRAVLASPVCATVTLDDDHAGIFTFECDTIHVSSEGIVME 549
 Db 321 QLSFSEAGLRIMITSHFP-PKTRLS---MASRMLINERQRLLNSRAYTGESEVAKIP 375
 Qy 550 VKLRTSGARGATIVPVRTVECTAKSGGEDDFDTYCBLEKNIDETVTRVKTIVDREYE 609
 Db 376 IKHTVENGT-GPSSAPDRGVNGTRR---DDIVATD-----NETENE 413
 Qy 610 RENFFIALGEKWKMERGISDVTDRKLTMEEPEAKRAEMGKPVLGEBHPKLEVIEESYE 669
 Db 414 NEEN-----ENNE-----EEPE----- 428
 Qy 670 FKTVDKLIKKNLALWVGTHSWRDQFMEAIVSAAGDEDDE-----SGE-ERLP 719
 Db 429 -----DEDDDEGPYPFDPPSGKETVK 451
 Qy 720 SCFDYVMHFLTVFWKVLIFACVVPTECHGW---ACFVAVSTLICMLTATGDLASHFG 774
 Db 452 WAFTPWLSF-----VLYFTVPCNPKH-WERKFWMTFASSTIWIASFAMVWMMYIIG 504
 Qy 775 CTIGKLSVATAVFVAFGTSVDPTEASKAAQDVFADASIGNVNGSNAVNFLGIGLAW 834
 Db 564 AJQTLAVDYGSYVIRLNRSRLGYISVGLLASYFVTFGVHLNKWQLDKKLGCGCLFLYGVF 563
 Qy 505 YTGIPDYMIGTFLAAGTSVDCMASLIVARQGM-GDMAYNSNSGSNVFDLILGGLPW 563
 Db 624 VCTSVL 873
 Qy 835 SVAAI-----YWALOGOEFHVSAQTIAFSV-----TLETFIAF 867
 Db 564 AJQTLAVDYGSYVIRLNRSRLGYISVGLLASYFVTFGVHLNKWQLDKKLGCGCLFLYGVF 623
 Db 624 LCFSIM 629

Search completed: November 30, 2002, 12:28:58
 Job time: 22.7346 secs